SEQUENCE LISTING

<110> Sewalt, Vincent
Hastings, Craig
Meeley, Robert
Hantke, Sabine
Jung, Rudolf
Everard, John
Allen, Stephen

<120> COMPOSITIONS AND METHODS FOR ALTERING THE DISULFIDE STATUS OF PROTEINS

<130> 5718-119 (035718/241421)

<150> 60/250,703
<151> 2000-12-01

<160> 25

<170> PatentIn version 3.0

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120

cgctactccg ctccccctca gtcctcagtt cctcacctag cggtagcgtg cgcgcgggag
180

acgtag atg gcg gct tcg gag gcg gca gcg gcg gcg gca aca ccg gtg
228
Met Ala Ala Ser Glu Ala Ala Ala Ala Ala Ala Thr Pro Val
1 5 10

acg ccg aca gag ggg acg gtg atc gcg atc cac agc ctg gag gag tgg
276
Thr Pro Thr Glu Gly Thr Val Ile Ala Ile His Ser Leu Glu Glu Trp
15 20 25 30

agc atc cag atc gag gag gcc aac agc gcc aag aag ctg gtg gtg att
324
Ser Ile Gln Ile Glu Glu Ala Asn Ser Ala Lys Lys Leu Val Val Ile
35 40 45

gac ttc act gca aca tgg tgt cct ccg tgc cgc gcc atg gct cca att
372
Asp Phe Thr Ala Thr Trp Cys Pro Pro Cys Arg Ala Met Ala Pro Ile

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            50                  55                  60

ttt gct gat atg gcc aag aag tcc cca aat gtt gtt ttc ctg aaa gtt
420
Phe Ala Asp Met Ala Lys Lys Ser Pro Asn Val Val Phe Leu Lys Val
        65                  70                  75

gat gtg gat gaa atg aag acc att gct gag caa ttc agc gta gag gcc
468
Asp Val Asp Glu Met Lys Thr Ile Ala Glu Gln Phe Ser Val Glu Ala
    80                  85                  90

atg cca aca ttc ctg ttc atg agg gag ggc gac gtc aag gac agg gtc
516
Met Pro Thr Phe Leu Phe Met Arg Glu Gly Asp Val Lys Asp Arg Val
95                  100                 105                 110

gtt ggc gca gca aag gaa gag cta gca agg aag ctt gaa cta cac atg
564
Val Gly Ala Ala Lys Glu Glu Leu Ala Arg Lys Leu Glu Leu His Met
                115                 120                 125

gcc tcg tag atcagtgatg ccgtaatgta gtattcgcct aaataagagg
613
Ala Ser


acgcctcgcc tcaactctga gaaaactagt gcttctgtga tggtaattcg tatgagagag
673

tgccccctttt ggtggtactt cttcgtatgt agtattaact cctgtcttaa tatgttgccc
733

tgcttgtgct tttcatacca tgtttgctct ttcagctgag gtgttaaaaa aaaaaaaaaa
793

aaaa
797


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<213>  Zea mays

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Thr Glu Gly Thr Val Ile Ala Ile His Ser Leu Glu Glu Trp Ser Ile
            20                  25                  30

Gln Ile Glu Glu Ala Asn Ser Ala Lys Lys Leu Val Val Ile Asp Phe
        35                  40                  45
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Thr Ala Thr Trp Cys Pro Pro Cys Arg Ala Met Ala Pro Ile Phe Ala
    50                  55                  60

Asp Met Ala Lys Lys Ser Pro Asn Val Val Phe Leu Lys Val Asp Val
65                  70                  75                  80

Asp Glu Met Lys Thr Ile Ala Glu Gln Phe Ser Val Glu Ala Met Pro
                85                  90                  95

Thr Phe Leu Phe Met Arg Glu Gly Asp Val Lys Asp Arg Val Val Gly
            100                 105                 110

Ala Ala Lys Glu Glu Leu Ala Arg Lys Leu Glu Leu His Met Ala Ser
        115                 120                 125
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agacgtag atg gcg gct tcg gag gcg gcg gcg gcg gcg gcg aca ccg gtg
110
        Met Ala Ala Ser Glu Ala Ala Ala Ala Ala Ala Thr Pro Val
        1               5                   10

gcg ccg aca gag ggg acg gtg atc gcg atc cac agc ctg gag gag tgg
158
Ala Pro Thr Glu Gly Thr Val Ile Ala Ile His Ser Leu Glu Glu Trp
15                  20                  25                  30

agc atc cag atc gag gag gcc aac agc gcc aag aag ctg gtg gtg att
206
Ser Ile Gln Ile Glu Glu Ala Asn Ser Ala Lys Lys Leu Val Val Ile
                35                  40                  45

gac ttc act gca aca tgg tgt cct ccg tgc cgc gcc atg gct cca att
254
Asp Phe Thr Ala Thr Trp Cys Pro Pro Cys Arg Ala Met Ala Pro Ile
            50                  55                  60

ttt gct gat atg gcc aag aag tcc cca aat gtt gtt ttc ctg aaa gtt
302
Phe Ala Asp Met Ala Lys Lys Ser Pro Asn Val Val Phe Leu Lys Val
        65                  70                  75

gat gtc gat gaa atg aag acc att gct gag caa ttc agc gta gag gcc
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T0602T 62h50001

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350
Asp Val Asp Glu Met Lys Thr Ile Ala Glu Gln Phe Ser Val Glu Ala
    80                  85                  90

atg cca aca ttc ctg ttc atg agg gag ggc gac gtc aag gac agg gtc
398
Met Pro Thr Phe Leu Phe Met Arg Glu Gly Asp Val Lys Asp Arg Val
95                  100                 105                 110

gtt ggc gca gca aag gaa gag cta gca agg aag ctt gaa cta cac atg
446
Val Gly Ala Ala Lys Glu Glu Leu Ala Arg Lys Leu Glu Leu His Met
                115                 120                 125

gcc tcg tag atcagtgatg ccgtaatgta gtattcgcct aaataagagg
495
Ala Ser


acgcctcgcc tcaactctga gaaaactagt gcttctgtga tggtaattcg tatgagagag
555

tgcccccttt ggtggtactt cttcgtatgt agtattaact cctgtcttaa tatgttgccc
615

tgcttgtgct tttcatacca tgtttgctct ttcagctgag gtgttatacg gtaaatcgga
675

gtcaatatct ttgaaattga ttaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa
735

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa
795

aaaa
799


<210>  4
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<212>  PRT
<213>  Zea mays

<400>  4

Met Ala Ala Ser Glu Ala Ala Ala Ala Ala Ala Thr Pro Val Ala Pro
1               5                   10                  15


Thr Glu Gly Thr Val Ile Ala Ile His Ser Leu Glu Glu Trp Ser Ile
            20                  25                  30


Gln Ile Glu Glu Ala Asn Ser Ala Lys Lys Leu Val Val Ile Asp Phe
        35                  40                  45


Thr Ala Thr Trp Cys Pro Pro Cys Arg Ala Met Ala Pro Ile Phe Ala
    50                  55                  60
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Asp Met Ala Lys Lys Ser Pro Asn Val Val Phe Leu Lys Val Asp Val
65                  70                  75                  80

Asp Glu Met Lys Thr Ile Ala Glu Gln Phe Ser Val Glu Ala Met Pro
                85                  90                  95

Thr Phe Leu Phe Met Arg Glu Gly Asp Val Lys Asp Arg Val Val Gly
            100                 105                 110

Ala Ala Lys Glu Glu Leu Ala Arg Lys Leu Glu Leu His Met Ala Ser
        115                 120                 125


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<212>  DNA
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47
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   1               5                  10                  15

gcg gag gtc gca agg aca tgg aag gta gag gcg atg cca acg ttc gta
95
Ala Glu Val Ala Arg Thr Trp Lys Val Glu Ala Met Pro Thr Phe Val
                20                  25                  30

ctt gtc aag gat ggg aag gag gta agc cgt gtg gtt ggg gcc aag aag
143
Leu Val Lys Asp Gly Lys Glu Val Ser Arg Val Val Gly Ala Lys Lys
            35                  40                  45

gac gag ctt gag agg aag atc cgg atg ttc acg tca tct tcc tca tcg
191
Asp Glu Leu Glu Arg Lys Ile Arg Met Phe Thr Ser Ser Ser Ser Ser
        50                  55                  60

taa actcctgtgg ttcgcctggg acggagttgc tgaagtgaaa tggtcccttc
244

tctcaatgct gaaaaaaggg ggaaaaacta tgtgaaaatg atggtagacg tgtctgggtc
304

agtaataaga gtttctaaaa tctgaatgag atttgaatcg ctttccgttg ctgaaaaaaa
364

aaa
367
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<210> 6
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<213> Zea mays

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Arg Phe Ser Asp Ala Ile Phe Val Lys Val Asp Val Asp Glu Leu Ala
1 5 10 15

Glu Val Ala Arg Thr Trp Lys Val Glu Ala Met Pro Thr Phe Val Leu
20 25 30

Val Lys Asp Gly Lys Glu Val Ser Arg Val Val Gly Ala Lys Lys Asp
35 40 45

Glu Leu Glu Arg Lys Ile Arg Met Phe Thr Ser Ser Ser Ser Ser
50 55 60

<210> 7
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1 5

acc tta gtg acg ccc cct ccg ccc gcc gcc gac gac ccg aac tgc gcc
103
Thr Leu Val Thr Pro Pro Pro Pro Ala Ala Asp Asp Pro Asn Cys Ala
10 15 20

gtg gtg gcc gcg cac tcc aag gcc acc tac gac gag cag tgg gcg gcc
151
Val Val Ala Ala His Ser Lys Ala Thr Tyr Asp Glu Gln Trp Ala Ala
25 30 35

cac aag agc agc agc aag ctg atg gtg atc gac ttc tcg gcg tcc tgg
199
His Lys Ser Ser Ser Lys Leu Met Val Ile Asp Phe Ser Ala Ser Trp
40 45 50

tgc ggg ccc tgc cgc ttc atc gag ccg gcc ttc aag gag ctg gcc tcc
247
Cys Gly Pro Cys Arg Phe Ile Glu Pro Ala Phe Lys Glu Leu Ala Ser
55 60 65 70

T0602F 62h5000T

cgc ttc acc gat gcc atc ttc atc aag gtc gac gtc gac gag ctc gcg
295
Arg Phe Thr Asp Ala Ile Phe Ile Lys Val Asp Val Asp Glu Leu Ala
75 80 85

gag gtc gca agg aca tgg aag gta gag gcg atg cca acg ttc gtg ctg
343
Glu Val Ala Arg Thr Trp Lys Val Glu Ala Met Pro Thr Phe Val Leu
90 95 100

gtc aag gat ggg aag gag gta ggc cgt gtg att ggg gct aag aag gac
391
Val Lys Asp Gly Lys Glu Val Gly Arg Val Ile Gly Ala Lys Lys Asp
105 110 115

gag ctt gag agg aag atc agg atg ttc gtc acg tca tct tcc tcg tcc
439
Glu Leu Glu Arg Lys Ile Arg Met Phe Val Thr Ser Ser Ser Ser Ser
120 125 130

taa cttagcagtg catacactcc caccttatta ctggtttctc gactccagtg
492

gttcgcctgg gacggggttg ctgaaatggt tcccttctct gaatactgaa aaatcaaaaa
552

aagaagtata tgaaaaaatg atggtagacg tgtctgggtc aataagagtt tctgaaactt
612

ggatttgtat gtgtcagtct ctgtgttctg tttccaagga atggatcatg tgagtttgga
672

atatagctgg aaatatgttg tgctgttaaa aaaaaaaaaa aaaaaaaa
720

10035429.120301

<210> 8
<211> 134
<212> PRT
<213> Zea mays

<400> 8

Met Gly Ser Phe Phe Ser Thr Leu Val Thr Pro Pro Pro Pro Ala Ala
1 5 10 15

Asp Asp Pro Asn Cys Ala Val Val Ala Ala His Ser Lys Ala Thr Tyr
20 25 30

Asp Glu Gln Trp Ala Ala His Lys Ser Ser Ser Lys Leu Met Val Ile
35 40 45

Asp Phe Ser Ala Ser Trp Cys Gly Pro Cys Arg Phe Ile Glu Pro Ala
50 55 60

```
Phe Lys Glu Leu Ala Ser Arg Phe Thr Asp Ala Ile Phe Ile Lys Val
65                  70                  75                  80

Asp Val Asp Glu Leu Ala Glu Val Ala Arg Thr Trp Lys Val Glu Ala
                85                  90                  95

Met Pro Thr Phe Val Leu Val Lys Asp Gly Lys Glu Val Gly Arg Val
            100                 105                 110

Ile Gly Ala Lys Lys Asp Glu Leu Glu Arg Lys Ile Arg Met Phe Val
        115                 120                 125

Thr Ser Ser Ser Ser Ser
    130
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T02021 62h5007

<210> 9
<211> 722
<212> DNA
<213> Zea mays

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<222> (84)..(455)

<400> 9

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ccaccgagga agaagagaga gga atg gcg tcc gag gag gaa gga gtc gtg atc
113
                          Met Ala Ser Glu Glu Glu Gly Val Val Ile
                          1               5                   10

gcc tgc cac acc aag gcc gac ttc gac gcc cac atg gcc aag gcc aag
161
Ala Cys His Thr Lys Ala Asp Phe Asp Ala His Met Ala Lys Ala Lys
            15                  20                  25

gag gcc ggc aag ctg gtg atc att gac ttc acg gcc tcc tgg tgc ggc
209
Glu Ala Gly Lys Leu Val Ile Ile Asp Phe Thr Ala Ser Trp Cys Gly
        30                  35                  40

ccc tgc cgc ttc atc gcg cca ctg ttc gtc gag cac gcc aag aag ttc
257
Pro Cys Arg Phe Ile Ala Pro Leu Phe Val Glu His Ala Lys Lys Phe
    45                  50                  55

acc cag gct gtg ttc ctg aag gtg gac gtg gac gag ctg aag gaa gtt
305
Thr Gln Ala Val Phe Leu Lys Val Asp Val Asp Glu Leu Lys Glu Val
60                  65                  70
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```
gcc gcg gcc tac gat gtc gag gcg atg ccg acc ttc cac ttc gtc aag
353
Ala Ala Ala Tyr Asp Val Glu Ala Met Pro Thr Phe His Phe Val Lys
75                  80                  85                  90

aac ggg gtg acg gtc gag acc gtc gtc ggt gcc agg aag gag aac ctc
401
Asn Gly Val Thr Val Glu Thr Val Val Gly Ala Arg Lys Glu Asn Leu
                95                  100                 105

ctg gcc cag atc gag aag cac tgc gcc gcg gcc gtg cct gct gcg tct
449
Leu Ala Gln Ile Glu Lys His Cys Ala Ala Ala Val Pro Ala Ala Ser
            110                 115                 120

gcg tag agaggatgga ccagcacgtg gcggtggcgg tggcggttgt cttgtcgttt
505
Ala


tcagtttggg cttgtcagct gtggctgggt ggttgattgt gaactggagc atgcagtttt
565

actctgggag cccatcattt ggttggctca ggtgtcaata atctgtatac cttaatcatg
625

gatagttgtt gtgagttgtg attggacttt ggaatttgga tgtctggctt cgttctgtta
685

tgatgatgat gatggattga aaaaaaaaaa aaaaaaa
722


<210>  10
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<212>  PRT
<213>  Zea mays

<400>  10

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1               5                   10                  15


Asp Phe Asp Ala His Met Ala Lys Ala Lys Glu Ala Gly Lys Leu Val
            20                  25                  30


Ile Ile Asp Phe Thr Ala Ser Trp Cys Gly Pro Cys Arg Phe Ile Ala
        35                  40                  45


Pro Leu Phe Val Glu His Ala Lys Lys Phe Thr Gln Ala Val Phe Leu
    50                  55                  60


Lys Val Asp Val Asp Glu Leu Lys Glu Val Ala Ala Ala Tyr Asp Val
65                  70                  75                  80
```


10059429 "12301

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Glu Ala Met Pro Thr Phe His Phe Val Lys Asn Gly Val Thr Val Glu
                85                  90                  95


Thr Val Val Gly Ala Arg Lys Glu Asn Leu Leu Ala Gln Ile Glu Lys
            100                 105                 110


His Cys Ala Ala Ala Val Pro Ala Ala Ser Ala
        115                 120


<210>  11
<211>  727
<212>  DNA
<213>  Zea mays

<220>
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<222>  (84)..(452)

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60

cgacaccgag gaagaagaga tca atg gcg tcc gag cag gga gtc gtg atc gcg
113
                          Met Ala Ser Glu Gln Gly Val Val Ile Ala
                          1               5                   10

tgc cac agc aag gct gag ttt gac gcc cac atg acc aag gcc cag gaa
161
Cys His Ser Lys Ala Glu Phe Asp Ala His Met Thr Lys Ala Gln Glu
                15                  20                  25

gcc ggc aag ctg gtg gtc att gac ttc act gcc gcc tgg tgc ggt cca
209
Ala Gly Lys Leu Val Val Ile Asp Phe Thr Ala Ala Trp Cys Gly Pro
            30                  35                  40

tgc cgc gcc atc gcc cca ctg ttc gtc gaa cac gcc aag aag ttc act
257
Cys Arg Ala Ile Ala Pro Leu Phe Val Glu His Ala Lys Lys Phe Thr
        45                  50                  55

cag gtc gtc ttc ctg aag gtg gac gtg gac gaa gtg aag gaa gtc acc
305
Gln Val Val Phe Leu Lys Val Asp Val Asp Glu Val Lys Glu Val Thr
    60                  65                  70

gcg gcc tac gag gtc gag gcg atg ccg acc ttc cac ttc gtc aag aac
353
Ala Ala Tyr Glu Val Glu Ala Met Pro Thr Phe His Phe Val Lys Asn
75                  80                  85                  90

ggc aag acg gtc gcg acc atc gtg ggt gcc aag aag gac gag ctc ctg
401
Gly Lys Thr Val Ala Thr Ile Val Gly Ala Lys Lys Asp Glu Leu Leu
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95 100 105

gcc cag atc gag aag cat gcc gcg cct gcg cct gcg tct gcg tct gcc
449
Ala Gln Ile Glu Lys His Ala Ala Pro Ala Pro Ala Ser Ala Ser Ala
110 115 120

taa aggagatcag atcagtcgtc gccgtcaata agggccagca cgtatggctg
502

taaatgttgt cgttatcagt tctggctttg tcgtttgtgg gcgattgtga actagtagta
562

tgtttgtttc tatccgagcc ggaggcgata cttaaccatg gatacttgtt gtgagttcgt
622

ttctgttcgc gtgtgactct tgaattgaat caaccagctc accactgcac caggccgtgg
682

tgagtggtga cagtgatttc ctgttaaaaa aaaaaaaaaa aaaaa
727

<210> 12
<211> 122
<212> PRT
<213> Zea mays

<400> 12

Met Ala Ser Glu Gln Gly Val Val Ile Ala Cys His Ser Lys Ala Glu
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Phe Asp Ala His Met Thr Lys Ala Gln Glu Ala Gly Lys Leu Val Val
20 25 30

Ile Asp Phe Thr Ala Ala Trp Cys Gly Pro Cys Arg Ala Ile Ala Pro
35 40 45

Leu Phe Val Glu His Ala Lys Lys Phe Thr Gln Val Val Phe Leu Lys
50 55 60

Val Asp Val Asp Glu Val Lys Glu Val Thr Ala Ala Tyr Glu Val Glu
65 70 75 80

Ala Met Pro Thr Phe His Phe Val Lys Asn Gly Lys Thr Val Ala Thr
85 90 95

Ile Val Gly Ala Lys Lys Asp Glu Leu Leu Ala Gln Ile Glu Lys His
100 105 110

Ala Ala Pro Ala Pro Ala Ser Ala Ser Ala

10021"624500T

115 120

<210> 13
<211> 700
<212> DNA
<213> Zea mays

<220>
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<222> (41)..(421)

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Met Ala Ala Glu Glu
1 5

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103
Gly Ala Val Ile Ala Cys His Thr Lys Asp Glu Phe Asp Ala Arg Met
10 15 20

gcc aag gcc aag gag cag ggc aag ctg gtg gtc atc gac ttc atg gcc
151
Ala Lys Ala Lys Glu Gln Gly Lys Leu Val Val Ile Asp Phe Met Ala
25 30 35

ccc tgg tgc agt ggg tgc cag atg atg gcc ccg gtg tac gcg gac tgc
199
Pro Trp Cys Ser Gly Cys Gln Met Met Ala Pro Val Tyr Ala Asp Cys
40 45 50

gcc agc aag tac cct tcc gcg gtc ttc ctc gag gtc gac gtc gac gaa
247
Ala Ser Lys Tyr Pro Ser Ala Val Phe Leu Glu Val Asp Val Asp Glu
55 60 65

ctg ctg gaa gtc gcg aag atc tac ggc gtc cat gtg atg ccg acc ttc
295
Leu Leu Glu Val Ala Lys Ile Tyr Gly Val His Val Met Pro Thr Phe
70 75 80 85

tgc ttc atc agg aac ggc gag acg ctc gag agc ttt gct acc gtc gac
343
Cys Phe Ile Arg Asn Gly Glu Thr Leu Glu Ser Phe Ala Thr Val Asp
90 95 100

gag gac gag ctc cgg gac gcc gtc agg aag tac gcc gcc gct ggc act
391
Glu Asp Glu Leu Arg Asp Ala Val Arg Lys Tyr Ala Ala Ala Gly Thr
105 110 115

acg acg gct cct gcc tcg gcg tcc gcc taa ttcaggagat gtgatgtgta
441
Thr Thr Ala Pro Ala Ser Ala Ser Ala
120 125

gcaaatagcg cgcgcgcacc agtcgtcaat aaataaataa ataaataaat aaataaataa

T0E021 "62h5001

501

ataaataaat aaaggccaac gtacgacgac aaattagtgg cgcgcgcggt agtagctagc
561

agagtatgcg ccgccactgt gtcgatctgc agtttggtcg tttaaaagtg attgtagtgt
621

gtactatgtt cagctcgaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa
681

aaaaaaaaaa aaaaaaaaa
700

<210> 14
<211> 126
<212> PRT
<213> Zea mays

<400> 14

Met Ala Ala Glu Glu Gly Ala Val Ile Ala Cys His Thr Lys Asp Glu
1 5 10 15

Phe Asp Ala Arg Met Ala Lys Ala Lys Glu Gln Gly Lys Leu Val Val
20 25 30

Ile Asp Phe Met Ala Pro Trp Cys Ser Gly Cys Gln Met Met Ala Pro
35 40 45

Val Tyr Ala Asp Cys Ala Ser Lys Tyr Pro Ser Ala Val Phe Leu Glu
50 55 60

Val Asp Val Asp Glu Leu Leu Glu Val Ala Lys Ile Tyr Gly Val His
65 70 75 80

Val Met Pro Thr Phe Cys Phe Ile Arg Asn Gly Glu Thr Leu Glu Ser
85 90 95

Phe Ala Thr Val Asp Glu Asp Glu Leu Arg Asp Ala Val Arg Lys Tyr
100 105 110

Ala Ala Ala Gly Thr Thr Thr Ala Pro Ala Ser Ala Ser Ala
115 120 125

<210> 15
<211> 658
<212> DNA
<213> Hordeum vulgare

EP 1624001 A2

<220>
<221> CDS
<222> (52)..(420)

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57
Met Ala
1

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105
Ala Ser Ala Thr Ala Ala Ala Val Ala Ala Glu Val Ile Ser Val His
5 10 15

agc ctg gag cag tgg acc atg cag atc gag gag gcc aac acc gcc aag
153
Ser Leu Glu Gln Trp Thr Met Gln Ile Glu Glu Ala Asn Thr Ala Lys
20 25 30

aag ctg gtg gtg att gac ttc act gca tca tgg tgc gga cca tgc cgc
201
Lys Leu Val Val Ile Asp Phe Thr Ala Ser Trp Cys Gly Pro Cys Arg
35 40 45 50

atc atg gct cca gtt ttc gct gat ctc gcc aag aag ttc cca aat gct
249
Ile Met Ala Pro Val Phe Ala Asp Leu Ala Lys Lys Phe Pro Asn Ala
55 60 65

gtt ttc ctc aag gtc gac gtg gat gaa ctg aag ccc att gct gag caa
297
Val Phe Leu Lys Val Asp Val Asp Glu Leu Lys Pro Ile Ala Glu Gln
70 75 80

ttc agt gtc gag gcc atg cca acg ttc ctg ttc atg aag gaa gga gac
345
Phe Ser Val Glu Ala Met Pro Thr Phe Leu Phe Met Lys Glu Gly Asp
85 90 95

gtc aag gac agg gtt gtc gga gct atc aag gag gaa ctg acc gcc aag
393
Val Lys Asp Arg Val Val Gly Ala Ile Lys Glu Glu Leu Thr Ala Lys
100 105 110

gtt ggg ctt cac gcg gcg gcc cag taa ttacctattg gtgtagtatt
440
Val Gly Leu His Ala Ala Ala Gln
115 120

cgcctaaata aaattgccgc tcaagaagac tatgaatgct gtgtactgct tgctacttgt
500

tgttggttta tggatactgc gatgcttgat ccaagctagt gtgcttttgc atatggttaa
560

ccaaaacagg attgctaaat cttagtcgac tgagatttaa ccaagtctta gtcaaagcta
620

tattggcgtg atcttacgta aaaaaaaaaa aaaaaaaa
658

<210> 16
<211> 122
<212> PRT
<213> Hordeum vulgare

<400> 16

Met Ala Ala Ser Ala Thr Ala Ala Ala Val Ala Ala Glu Val Ile Ser
1 5 10 15

Val His Ser Leu Glu Gln Trp Thr Met Gln Ile Glu Glu Ala Asn Thr
20 25 30

Ala Lys Lys Leu Val Val Ile Asp Phe Thr Ala Ser Trp Cys Gly Pro
35 40 45

Cys Arg Ile Met Ala Pro Val Phe Ala Asp Leu Ala Lys Lys Phe Pro
50 55 60

Asn Ala Val Phe Leu Lys Val Asp Val Asp Glu Leu Lys Pro Ile Ala
65 70 75 80

Glu Gln Phe Ser Val Glu Ala Met Pro Thr Phe Leu Phe Met Lys Glu
85 90 95

Gly Asp Val Lys Asp Arg Val Val Gly Ala Ile Lys Glu Glu Leu Thr
100 105 110

Ala Lys Val Gly Leu His Ala Ala Ala Gln
115 120

<210> 17
<211> 580
<212> DNA
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<220>
<221> misc_feature
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486, 493, 501, 507, 515, 519, 532, 542, and 579 can be an a, c, g, or t

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60

10005429.120301

agggtgccgt gatcgcgtgc cacaccaagg acgagttcga cgcccgcatg gccaangncn
120

aggancnggc aagctggtgg tcatcgactt catggccccc tggtgcagtg ggtgccagat
180

gatggccccg gtgtacgcgg actgcgccag caagtaccct tccgcggtct tcctcgaggt
240

cgacgtggac gaactgctgg aagtcgcgaa gatctacggc gtccatgtga tgccgacctt
300

ctgcttcatc aggaacngcg agacgctcga nagctttgct accgtcgacg aagacgagct
360

ccgggacgcc gtcaggaagt acgccgccgc tggcactacg acgctcctgc ctcggcgtcc
420

gcctaattca gganatgtga tgtgtagcaa atagcgcgcg cgcaccatcg tcnataaata
480

antaantaat aantaattaa ntaantnaag ggccncgtnc aacaacaatt tntggccccg
540

cngtattact acaaatttgc ccccccctgtt tcatctgcnt
580

<210> 18
<211> 590
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (60)..(425)

<220>
<221> misc_feature
<223> "n" at position 9, 493, 537, 548, 581, and 584 can be an a, c, g,
or t

<400> 18
gttgcaatna caacgaacag aagctctcga tctcaccgac accgaggaag aagagatca
59

atg gcg tcc gag cag gga gtc gtg atc gcg tgc cac agc aag gct gag
107
Met Ala Ser Glu Gln Gly Val Val Ile Ala Cys His Ser Lys Ala Glu
1 5 10 15

ttc gac gcc cac atg acc aag gcc cag gaa gcc ggc aag ctg gtg gtc
155
Phe Asp Ala His Met Thr Lys Ala Gln Glu Ala Gly Lys Leu Val Val
20 25 30

TOE021"62h5000T

atc gac ttc act gcc gcc tgg tgc ggt cca tgc cgc gcc atc gcc cca
203
Ile Asp Phe Thr Ala Ala Trp Cys Gly Pro Cys Arg Ala Ile Ala Pro
35 40 45

ctg ttc gtc gaa cac gcc aag aag ttc act cag gtc gtc ttc ctg aag
251
Leu Phe Val Glu His Ala Lys Lys Phe Thr Gln Val Val Phe Leu Lys
50 55 60

gtg gac gtg gac gaa gtg aag gaa gtc acc gcg gcc tac gag gtc gag
299
Val Asp Val Asp Glu Val Lys Glu Val Thr Ala Ala Tyr Glu Val Glu
65 70 75 80

gcg atg ccg acc ttc cac ttc gtc aag aac ggc aag acg gtc gcg acc
347
Ala Met Pro Thr Phe His Phe Val Lys Asn Gly Lys Thr Val Ala Thr
85 90 95

atc gtg ggt gcc agg aag gac gag ctc ctg gcc cag atc gag aag cat
395
Ile Val Gly Ala Arg Lys Asp Glu Leu Leu Ala Gln Ile Glu Lys His
100 105 110

gcc gcg cct gcg cct gcg tct gcg tct gcc taaaggagat cagtcgtcgc
445
Ala Ala Pro Ala Pro Ala Ser Ala Ser Ala
115 120

cgtcaataag ggccagcacg tatggctgta aatgttgtcg ttatcagntc tggctttgtc
505

gtttgtgggc gattgtgaac tagtagtatg tnggttctat ccnaagccgg aggcgatctt
565

aacctgggat acttgntgng aaaaa
590

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<210> 19
<211> 122
<212> PRT
<213> Zea mays

<220>
<221> misc_feature
<223> "n" at position 9, 493, 537, 548, 581, and 584 can be an a, c, g,
or t

<400> 19

Met Ala Ser Glu Gln Gly Val Val Ile Ala Cys His Ser Lys Ala Glu
1 5 10 15

Phe Asp Ala His Met Thr Lys Ala Gln Glu Ala Gly Lys Leu Val Val
20 25 30

Ile Asp Phe Thr Ala Ala Trp Cys Gly Pro Cys Arg Ala Ile Ala Pro
35 40 45

Leu Phe Val Glu His Ala Lys Lys Phe Thr Gln Val Val Phe Leu Lys
50 55 60

Val Asp Val Asp Glu Val Lys Glu Val Thr Ala Ala Tyr Glu Val Glu
65 70 75 80

Ala Met Pro Thr Phe His Phe Val Lys Asn Gly Lys Thr Val Ala Thr
85 90 95

Ile Val Gly Ala Arg Lys Asp Glu Leu Leu Ala Gln Ile Glu Lys His
100 105 110

Ala Ala Pro Ala Pro Ala Ser Ala Ser Ala
115 120

<210> 20
<211> 948
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (3)..(737)

<400> 20
cc aag atc ctc acc gag acc gtc acc acc gtg gac ttc tcc gcc cgc
47
Lys Ile Leu Thr Glu Thr Val Thr Thr Val Asp Phe Ser Ala Arg
1 5 10 15

ccc ttc cgt gtc gcc tcc gac gac acc gtt gtg cac gcc gac tcc gtc
95
Pro Phe Arg Val Ala Ser Asp Asp Thr Val Val His Ala Asp Ser Val
20 25 30

gtc gtc gcc acg ggc gcc gtc gcg cgc agg ctg cac ttc gcc ggc tcc
143
Val Val Ala Thr Gly Ala Val Ala Arg Arg Leu His Phe Ala Gly Ser
35 40 45

gac gcc ttc tgg aac cgg ggc atc tcc gcc tgc gcc gtc tgc gac ggg
191
Asp Ala Phe Trp Asn Arg Gly Ile Ser Ala Cys Ala Val Cys Asp Gly
50 55 60

gct gcg cct atc ttc cgg aac aag ccc atc gcc gtc gtc gga ggc ggg
239
Ala Ala Pro Ile Phe Arg Asn Lys Pro Ile Ala Val Val Gly Gly Gly

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    65                  70                  75

gac tcc gcc atg gag gag gct aac ttc ctc acc aag tac ggc tcg caa
287
Asp Ser Ala Met Glu Glu Ala Asn Phe Leu Thr Lys Tyr Gly Ser Gln
80                  85                  90                  95

gtt tac atc atc cac cgc cgc agc gac ttc cgg gcg tcc aag atc atg
335
Val Tyr Ile Ile His Arg Arg Ser Asp Phe Arg Ala Ser Lys Ile Met
                100                 105                 110

cag gcg cgc acg ctc tcc aac ccc aag atc aag gtc gtc tgg aac tcc
383
Gln Ala Arg Thr Leu Ser Asn Pro Lys Ile Lys Val Val Trp Asn Ser
            115                 120                 125

gag gtc gtc gag gcc tac ggc ggt gcg gat ggc ggc ccg cta gcc ggc
431
Glu Val Val Glu Ala Tyr Gly Gly Ala Asp Gly Gly Pro Leu Ala Gly
        130                 135                 140

gtc aag gtc aag gac gtc gtc acc ggc gag gtc tct gat ctc cag gtg
479
Val Lys Val Lys Asp Val Val Thr Gly Glu Val Ser Asp Leu Gln Val
    145                 150                 155

gcc ggg ctc ttc ttt gcc atc ggt cac gag ccg gcg aca aaa ttt ctt
527
Ala Gly Leu Phe Phe Ala Ile Gly His Glu Pro Ala Thr Lys Phe Leu
160                 165                 170                 175

gga ggg cag ctc gag ctc gac tct gat ggg tat gtg gtg acc aag ccc
575
Gly Gly Gln Leu Glu Leu Asp Ser Asp Gly Tyr Val Val Thr Lys Pro
                180                 185                 190

ggt tcc acg cac acc agt gtg cag ggg gtc ttt gca gct ggg gat gtc
623
Gly Ser Thr His Thr Ser Val Gln Gly Val Phe Ala Ala Gly Asp Val
            195                 200                 205

cag gac aag aag tac cgc cag gcc att act gca gct gga tca ggt tgc
671
Gln Asp Lys Lys Tyr Arg Gln Ala Ile Thr Ala Ala Gly Ser Gly Cys
        210                 215                 220

atg gct gct ctg gat gca gag cac tac ctg cag gag gtt gga gca cag
719
Met Ala Ala Leu Asp Ala Glu His Tyr Leu Gln Glu Val Gly Ala Gln
    225                 230                 235

gaa ggg aag acc gat tga ctatgtctgg gccaagctgc tcttgggcca
767
Glu Gly Lys Thr Asp
240

aggaaaactt ctccgaaagc cgctctctag tggtgtaaac agcacattat tatttggttt
827
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T0E027'629450001

taggcctcaa attacgttac attggaaatt gatttatatg agcgtgcgca agcttgtata
887

cattattcgc attgtttatt actcttagag tcttagtcat taatcacact ttgctaaaaa
947

a
948

<210> 21
<211> 244
<212> PRT
<213> Zea mays

<400> 21

Lys Ile Leu Thr Glu Thr Val Thr Thr Val Asp Phe Ser Ala Arg Pro
1 5 10 15

Phe Arg Val Ala Ser Asp Asp Thr Val Val His Ala Asp Ser Val Val
20 25 30

Val Ala Thr Gly Ala Val Ala Arg Arg Leu His Phe Ala Gly Ser Asp
35 40 45

Ala Phe Trp Asn Arg Gly Ile Ser Ala Cys Ala Val Cys Asp Gly Ala
50 55 60

Ala Pro Ile Phe Arg Asn Lys Pro Ile Ala Val Val Gly Gly Gly Asp
65 70 75 80

Ser Ala Met Glu Glu Ala Asn Phe Leu Thr Lys Tyr Gly Ser Gln Val
85 90 95

Tyr Ile Ile His Arg Arg Ser Asp Phe Arg Ala Ser Lys Ile Met Gln
100 105 110

Ala Arg Thr Leu Ser Asn Pro Lys Ile Lys Val Val Trp Asn Ser Glu
115 120 125

Val Val Glu Ala Tyr Gly Gly Ala Asp Gly Gly Pro Leu Ala Gly Val
130 135 140

Lys Val Lys Asp Val Val Thr Gly Glu Val Ser Asp Leu Gln Val Ala
145 150 155 160

Gly Leu Phe Phe Ala Ile Gly His Glu Pro Ala Thr Lys Phe Leu Gly

10055269 - 120204

165 170 175

Gly Gln Leu Glu Leu Asp Ser Asp Gly Tyr Val Val Thr Lys Pro Gly
180 185 190

Ser Thr His Thr Ser Val Gln Gly Val Phe Ala Ala Gly Asp Val Gln
195 200 205

Asp Lys Lys Tyr Arg Gln Ala Ile Thr Ala Ala Gly Ser Gly Cys Met
210 215 220

Ala Ala Leu Asp Ala Glu His Tyr Leu Gln Glu Val Gly Ala Gln Glu
225 230 235 240

Gly Lys Thr Asp

<210> 22
<211> 556
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (1)..(336)

<400> 22
ggc ggt gcg gat ggc ggc ccg cta gcc ggc gtc aag gtc aag gac gtc
48
Gly Gly Ala Asp Gly Gly Pro Leu Ala Gly Val Lys Val Lys Asp Val
1 5 10 15

gtc acc ggc gag gtc tct gat ctc cag gtg gcc ggg ctc ttc ttt gcc
96
Val Thr Gly Glu Val Ser Asp Leu Gln Val Ala Gly Leu Phe Phe Ala
20 25 30

atc ggt cac gag ccg gcg aca aaa ttt ctt gga ggg cag ctc gag ctc
144
Ile Gly His Glu Pro Ala Thr Lys Phe Leu Gly Gly Gln Leu Glu Leu
35 40 45

gac tct gat ggg tat gtg gtg ccc aag ccc ggt tcc acg cac acc agt
192
Asp Ser Asp Gly Tyr Val Val Pro Lys Pro Gly Ser Thr His Thr Ser
50 55 60

gtg cag ggg gtc ttt gca gct ggg gat gtc cag gac aag aag tac cgc
240
Val Gln Gly Val Phe Ala Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg
65 70 75 80

cag gcc att act gca gct gga tca ggt tgc atg gct gct ctg gat gca

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288
Gln Ala Ile Thr Ala Ala Gly Ser Gly Cys Met Ala Ala Leu Asp Ala
85 90 95

gag cac tac ctg cag gag gtt gga gca cag gaa ggg aag acc gat tga
336
Glu His Tyr Leu Gln Glu Val Gly Ala Gln Glu Gly Lys Thr Asp
100 105 110

ctatgtctgg gccaagctgc tcttgggcca aggaaaactt ctccgaaagc cgctctctag
396

tggtgtaaac agcacattat tatttggttt taggcctcaa attacgttac attggaaatt
456

gatttatatg agcgtgcgca agcttgtata cattattcgc attgtttatt actcttagag
516

tcttagtcat taatcacact ttgctaaaaa aaaaaaaaaa
556

<210> 23
<211> 111
<212> PRT
<213> Zea mays

<400> 23

Gly Gly Ala Asp Gly Gly Pro Leu Ala Gly Val Lys Val Lys Asp Val
1 5 10 15

Val Thr Gly Glu Val Ser Asp Leu Gln Val Ala Gly Leu Phe Phe Ala
20 25 30

Ile Gly His Glu Pro Ala Thr Lys Phe Leu Gly Gly Gln Leu Glu Leu
35 40 45

Asp Ser Asp Gly Tyr Val Val Pro Lys Pro Gly Ser Thr His Thr Ser
50 55 60

Val Gln Gly Val Phe Ala Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg
65 70 75 80

Gln Ala Ile Thr Ala Ala Gly Ser Gly Cys Met Ala Ala Leu Asp Ala
85 90 95

Glu His Tyr Leu Gln Glu Val Gly Ala Gln Glu Gly Lys Thr Asp
100 105 110

<210> 24
<211> 1336

TOE021"62450001

<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (91)..(1086)

<400> 24
gaactgtaat ttcagatttc agagcgcgca agaacctct tgaccaccgc cgccgccgcc
60

gcgaagccaa gccaaactga gtaagcagct atg gag gga tcc gcc gcc gct ccg
114
Met Glu Gly Ser Ala Ala Ala Pro
1 5

ctc cgc acg cgc atc tgc atc atc ggg agc ggt ccc gct gcg cac acg
162
Leu Arg Thr Arg Ile Cys Ile Ile Gly Ser Gly Pro Ala Ala His Thr
10 15 20

gca gcc atc tac gcg gcc cgc gcg gag ctc aag cct gtg ctc ttc gag
210
Ala Ala Ile Tyr Ala Ala Arg Ala Glu Leu Lys Pro Val Leu Phe Glu
25 30 35 40

ggc tgg atg gcc aac gac atc gcc gcg ggc ggg cag ctc acc acc acc
258
Gly Trp Met Ala Asn Asp Ile Ala Ala Gly Gly Gln Leu Thr Thr Thr
45 50 55

acc gac gtc gag aac ttc ccg ggc ttc ccc aac ggc atc atg ggc gcc
306
Thr Asp Val Glu Asn Phe Pro Gly Phe Pro Asn Gly Ile Met Gly Ala
60 65 70

gac ctc atg gac aac tgc cgc gcg cag tcc ctg cgc ttt ggc acc aac
354
Asp Leu Met Asp Asn Cys Arg Ala Gln Ser Leu Arg Phe Gly Thr Asn
75 80 85

atc ctc tcc gag acc gtc acc gcc gtc gac ttt tcg gcc tgc cca ttc
402
Ile Leu Ser Glu Thr Val Thr Ala Val Asp Phe Ser Ala Cys Pro Phe
90 95 100

cga gtt agt gca gac tcc aca acc gtc ctc gcc gat gcg gtt atc gtt
450
Arg Val Ser Ala Asp Ser Thr Thr Val Leu Ala Asp Ala Val Ile Val
105 110 115 120

gcc acg gga gcc gtc gcg cgg cgc ctc cac ttc ccc ggg tcc gat gca
498
Ala Thr Gly Ala Val Ala Arg Arg Leu His Phe Pro Gly Ser Asp Ala
125 130 135

tac tgg aac cgc ggc atc tcc gcc tgt gcc gtc tgt gac ggt gcc gcc
546
Tyr Trp Asn Arg Gly Ile Ser Ala Cys Ala Val Cys Asp Gly Ala Ala

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            140                 145                 150

ccc atc ttc cgt aac aag ccc atc gcc gtc ata ggc ggc ggc gac tcc
594
Pro Ile Phe Arg Asn Lys Pro Ile Ala Val Ile Gly Gly Gly Asp Ser
        155                 160                 165

gct atg gag gag tcc aat ttc ctc acc aag tac ggc tcc cac gtc tac
642
Ala Met Glu Glu Ser Asn Phe Leu Thr Lys Tyr Gly Ser His Val Tyr
    170                 175                 180

atc atc cac cgc cgc aat acc ttc cgt gct tcc aag atc atg cag gcc
690
Ile Ile His Arg Arg Asn Thr Phe Arg Ala Ser Lys Ile Met Gln Ala
185                 190                 195                 200

agg gcg ctt gag aac ccc aaa att aag gtc ctc tgg gac tcg gaa gtt
738
Arg Ala Leu Glu Asn Pro Lys Ile Lys Val Leu Trp Asp Ser Glu Val
                205                 210                 215

gtc gag gcc tat ggc ggc gca aac ggc ggc cca ttg gct ggc gta aag
786
Val Glu Ala Tyr Gly Gly Ala Asn Gly Gly Pro Leu Ala Gly Val Lys
            220                 225                 230

gtt aag aac cta ctg aat ggt gag gtc tcg gat ctt cag gtg tct ggc
834
Val Lys Asn Leu Leu Asn Gly Glu Val Ser Asp Leu Gln Val Ser Gly
        235                 240                 245

ctc ttc ttc gcc atc ggg cat gag ccg gcg acc aaa ttc ctg ggc gga
882
Leu Phe Phe Ala Ile Gly His Glu Pro Ala Thr Lys Phe Leu Gly Gly
    250                 255                 260

cag ctt gaa ctc gat tca gat ggt tat gtg gaa acc aag cca ggt tcc
930
Gln Leu Glu Leu Asp Ser Asp Gly Tyr Val Glu Thr Lys Pro Gly Ser
265                 270                 275                 280

act cac acc agt gta aag ggt gta ttt gct gct ggc gac gtg cag gac
978
Thr His Thr Ser Val Lys Gly Val Phe Ala Ala Gly Asp Val Gln Asp
                285                 290                 295

aag aag tac cgt cag gcc att act gcc gct gga tca ggg tgc atg gct
1026
Lys Lys Tyr Arg Gln Ala Ile Thr Ala Ala Gly Ser Gly Cys Met Ala
            300                 305                 310

gca ttg gac gct gag cac tac ctg cag gag atc ggt gca cag gag gga
1074
Ala Leu Asp Ala Glu His Tyr Leu Gln Glu Ile Gly Ala Gln Glu Gly
        315                 320                 325

aag tct gat tga ctatatttag gtgtagcaac cagcaatcca tcgaatagtc
1126
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Lys Ser Asp
330

agttgtcggt gctgaaagcc gctctctgat gcgcgtttat gccatgggtt gtcatgagct
1186

cacgattgag atacctgatg atttatgctg cttagtagca tgctattctt atcgttagga
1246

tccagaagta tgtctgaact ctgaactatt tactggatac ctattcgtga ttactgcctt
1306

gaagtttttc cttagatatc aaaaaaaaaa
1336

<210> 25
<211> 331
<212> PRT
<213> Zea mays

<400> 25

Met Glu Gly Ser Ala Ala Ala Pro Leu Arg Thr Arg Ile Cys Ile Ile
1 5 10 15

Gly Ser Gly Pro Ala Ala His Thr Ala Ala Ile Tyr Ala Ala Arg Ala
20 25 30

Glu Leu Lys Pro Val Leu Phe Glu Gly Trp Met Ala Asn Asp Ile Ala
35 40 45

Ala Gly Gly Gln Leu Thr Thr Thr Thr Asp Val Glu Asn Phe Pro Gly
50 55 60

Phe Pro Asn Gly Ile Met Gly Ala Asp Leu Met Asp Asn Cys Arg Ala
65 70 75 80

Gln Ser Leu Arg Phe Gly Thr Asn Ile Leu Ser Glu Thr Val Thr Ala
85 90 95

Val Asp Phe Ser Ala Cys Pro Phe Arg Val Ser Ala Asp Ser Thr Thr
100 105 110

Val Leu Ala Asp Ala Val Ile Val Ala Thr Gly Ala Val Ala Arg Arg
115 120 125

Leu His Phe Pro Gly Ser Asp Ala Tyr Trp Asn Arg Gly Ile Ser Ala
130 135 140

EO021*62450004

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Cys Ala Val Cys Asp Gly Ala Ala Pro Ile Phe Arg Asn Lys Pro Ile
145                 150                 155                 160

Ala Val Ile Gly Gly Gly Asp Ser Ala Met Glu Glu Ser Asn Phe Leu
                165                 170                 175

Thr Lys Tyr Gly Ser His Val Tyr Ile Ile His Arg Arg Asn Thr Phe
            180                 185                 190

Arg Ala Ser Lys Ile Met Gln Ala Arg Ala Leu Glu Asn Pro Lys Ile
        195                 200                 205

Lys Val Leu Trp Asp Ser Glu Val Val Glu Ala Tyr Gly Gly Ala Asn
    210                 215                 220

Gly Gly Pro Leu Ala Gly Val Lys Val Lys Asn Leu Leu Asn Gly Glu
225                 230                 235                 240

Val Ser Asp Leu Gln Val Ser Gly Leu Phe Phe Ala Ile Gly His Glu
                245                 250                 255

Pro Ala Thr Lys Phe Leu Gly Gly Gln Leu Glu Leu Asp Ser Asp Gly
            260                 265                 270

Tyr Val Glu Thr Lys Pro Gly Ser Thr His Thr Ser Val Lys Gly Val
        275                 280                 285

Phe Ala Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg Gln Ala Ile Thr
    290                 295                 300

Ala Ala Gly Ser Gly Cys Met Ala Ala Leu Asp Ala Glu His Tyr Leu
305                 310                 315                 320

Gln Glu Ile Gly Ala Gln Glu Gly Lys Ser Asp
                325                 330
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